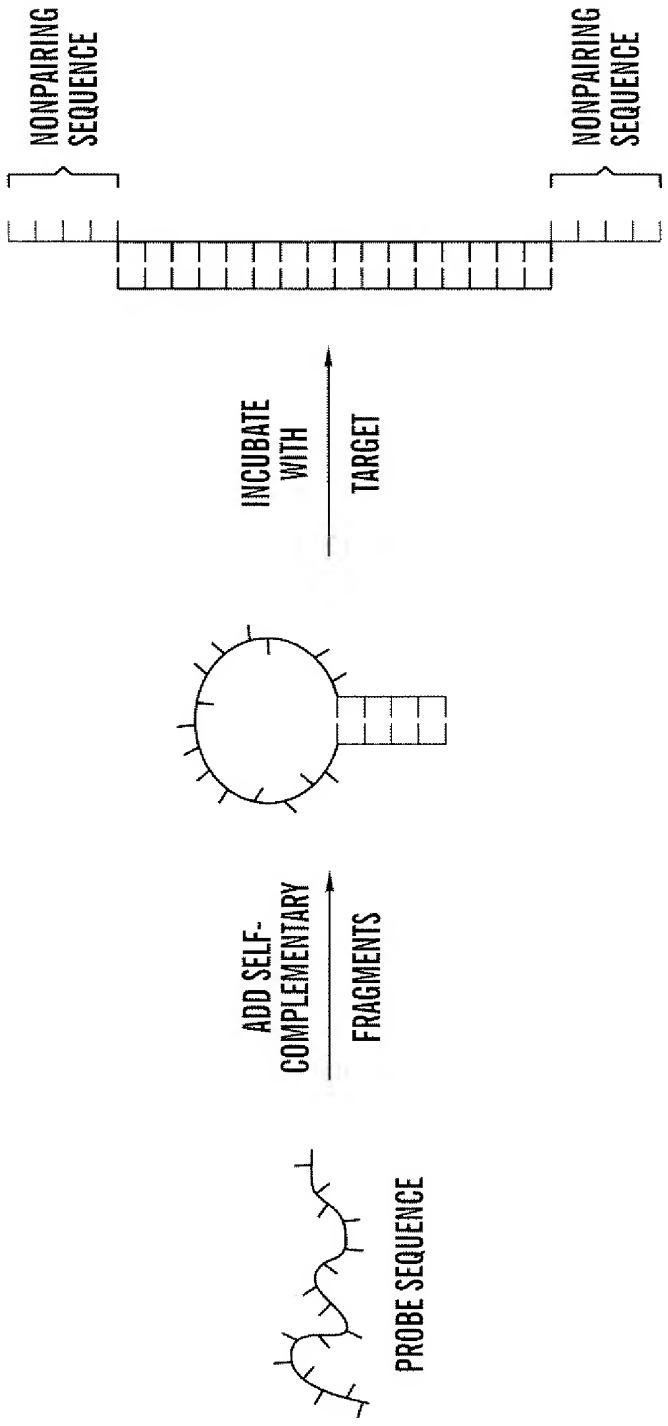


FIG. 1
PRIOR ART

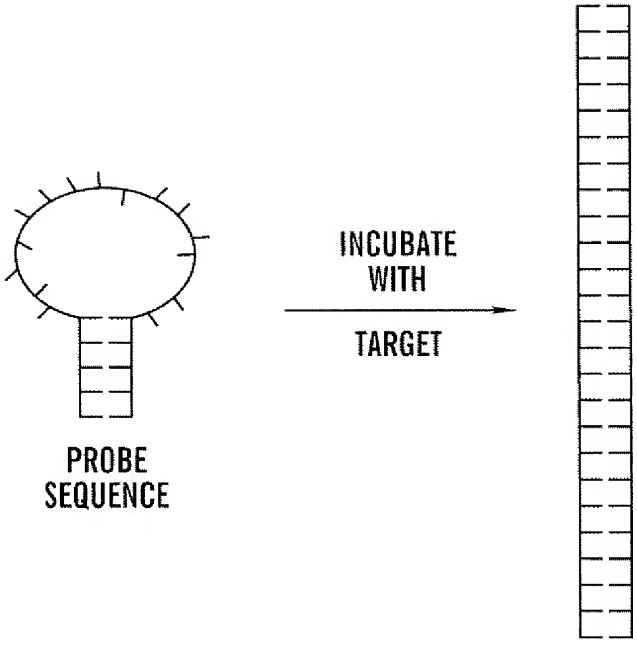


FIG. 2

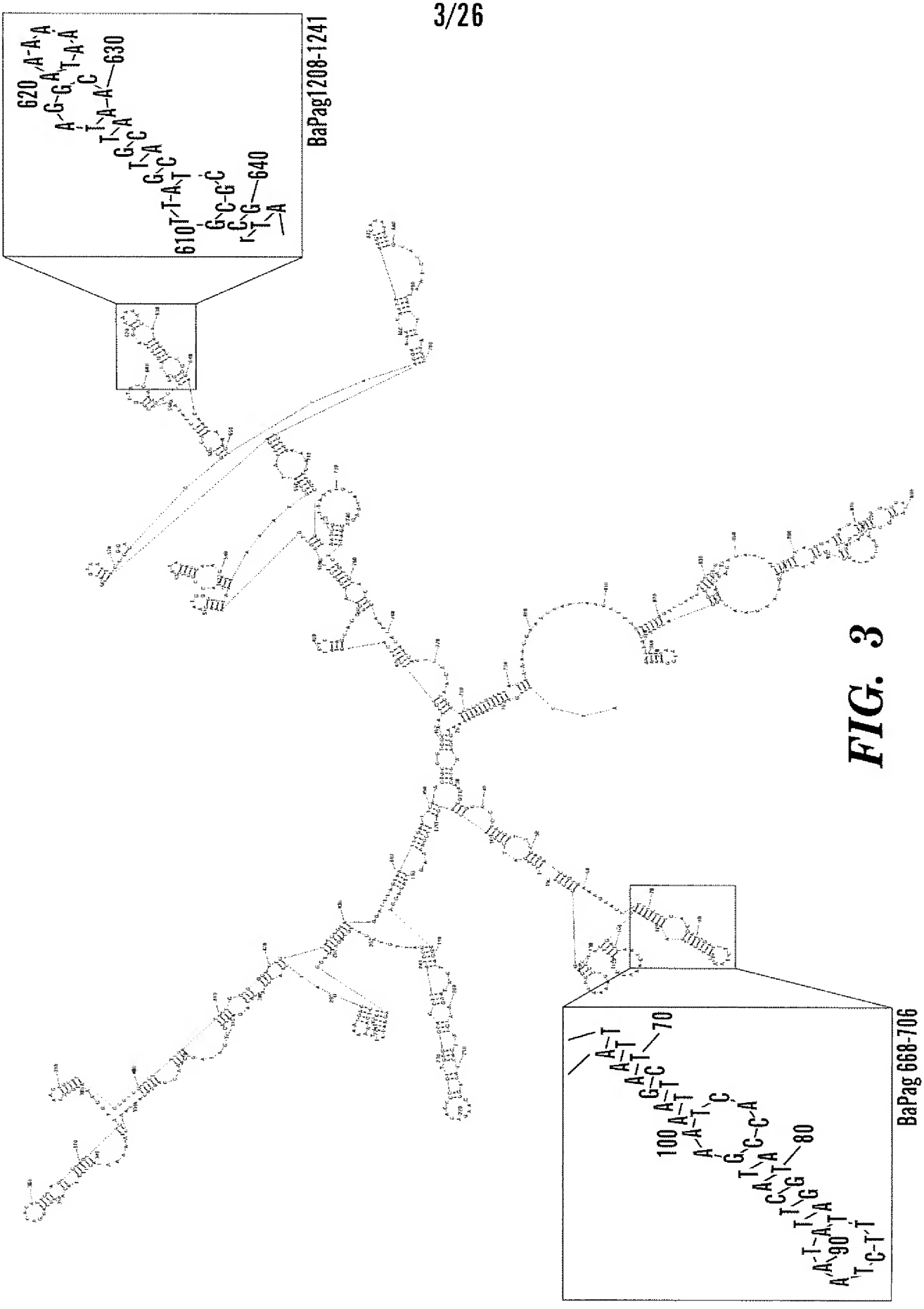
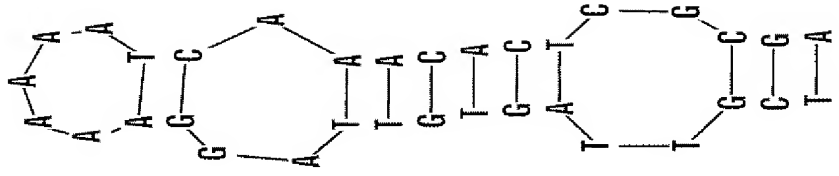


FIG. 3



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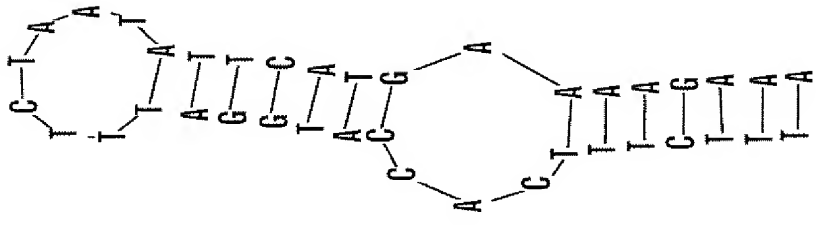
$E_{predict}$ = -4.7 kcal/mol

nt COUNT = 34

FIG. 4B



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$E_{predict}$ = -4.4 kcal/mol

nt COUNT = 39

FIG. 4A

Sequences producing significant alignments:	Score (bits)	E Value
gi|20520075|gb|AE011190.1| Bacillus anthracis str. A2012 pl...	78	7e-13
gi|16031494|emb|AJ413937.1|BAN413937 Bacillus anthracis par...	78	7e-13
gi|16031492|emb|AJ413936.1|BAN413936 Bacillus anthracis par...	78	7e-13
gi|9280532|gb|AF268967.1|AF268967 B acillus anthracis plasmi...	78	7e-13
gi|4894216|gb|AF065404.1| Bacillus anthracis virulence plas...	78	7e-13
gi|10880952|gb|AF306783.1| Bacillus anthracis isolate BA102...	78	7e-13
gi|10880950|gb|AF306782.1| Bacillus anthracis plasmid pX01 ...	78	7e-13
gi|10880948|gb|AF306781.1| Bacillus anthracis isolate 33 pr...	78	7e-13
gi|10880946|gb|AF306780.1| Bacillus anthracis isolate BA103...	78	7e-13
gi|10880944|gb|AF306779.1| Bacillus anthracis isolate 28 pr...	78	7e-13
gi|10880942|gb|AF306778.1| Bacillus anthracis plasmid pX01 ...	78	7e-13
gi|143280|gb|M22589.1|BACPAG Bacillus anthracis cryptic pro...	78	7e-13
gi|18308294|gb|AC104301.2| Homo sapiens chromosome 3 clone ...	42	0.038
gi|19033969|gb|AC069286.7| Homo sapiens BAC clone RP11-261N...	40	0.15
gi|34849950|gb|AC107065.5| Bos taurus clone rp42-513g13, co...	40	0.15
gi|30962756|gb|AC137820.11| Medicago truncatula clone mth2-...	38	0.60
gi|30522931|gb|AC123948.4| Mus musculus chromosome 10 clone...	38	0.60
gi|22552809|emb|AL671857.16| Mouse DNA sequence from clone ...	38	0.60
gi|11414543|emb|AL355352.16| Human DNA sequence from clone ...	38	0.60
gi|7768715|dbj|AP001713.1| Homo sapiens genomic DNA, chromo...	38	0.60
gi|4827077|dbj|AP000178.1| Homo sapiens genomic DNA, chromo...	38	0.60
gi|4835635|dbj|AP000266.1| Homo sapiens genomic DNA, chromo...	38	0.60
gi|3132344|dbj|AP000034.1| Homo sapiens genomic DNA, chromo...	38	0.60
gi|4730836|dbj|AP000102.1 Homo sapiens genomic DNA of 21q2 ...	38	0.60
gi|3947430|gb|AC003090.1| Homo sapiens BAC clone CTA-241I2 ...	36	2.4

FIG. 5

NEW SHEET

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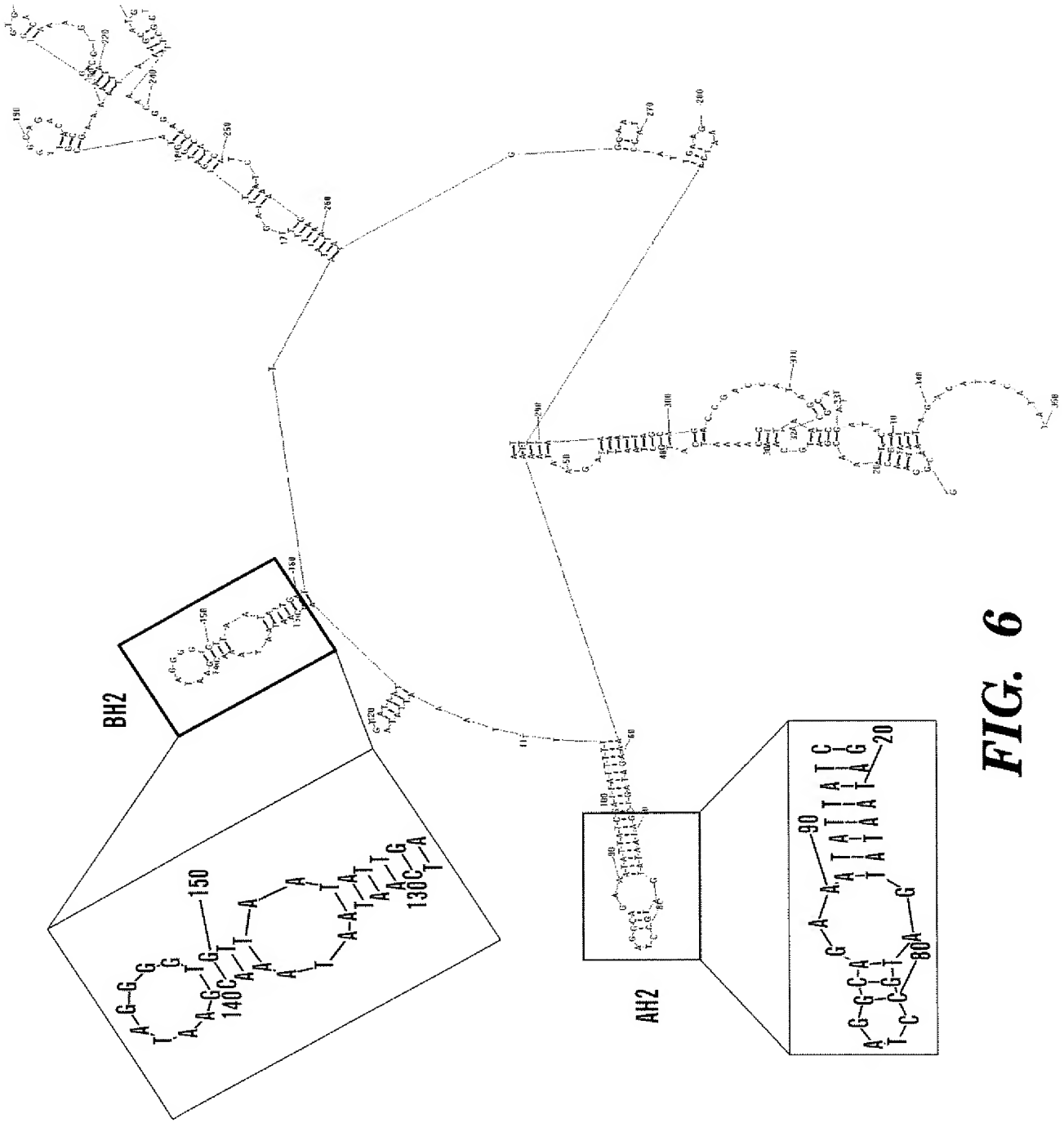
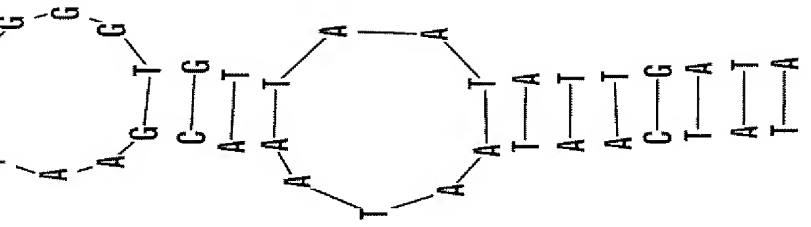


FIG. 6

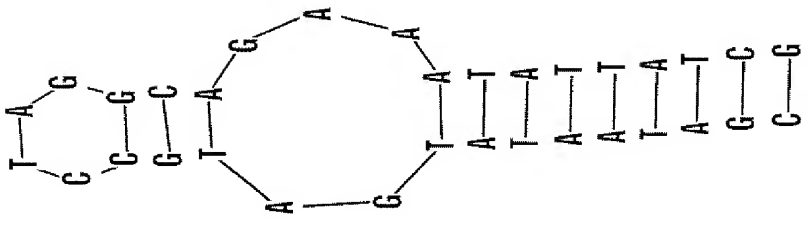


BH2

($E_{predict}$ = -3.5 kcal/mol)

nt=37

FIG. 7B



AH2

($E_{predict}$ = -6.1 kcal/mol)

nt=33

FIG. 7A

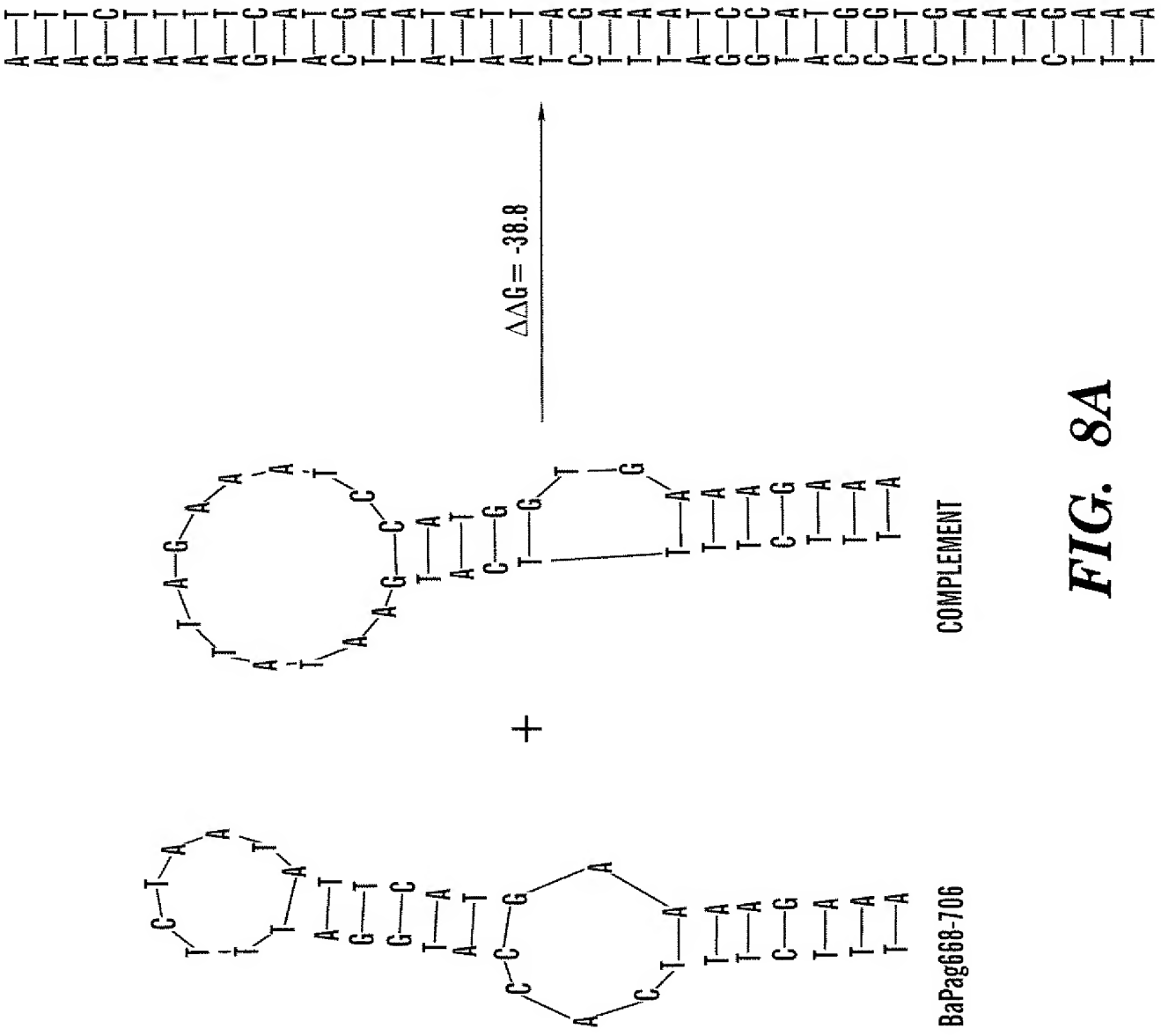


FIG. 8A

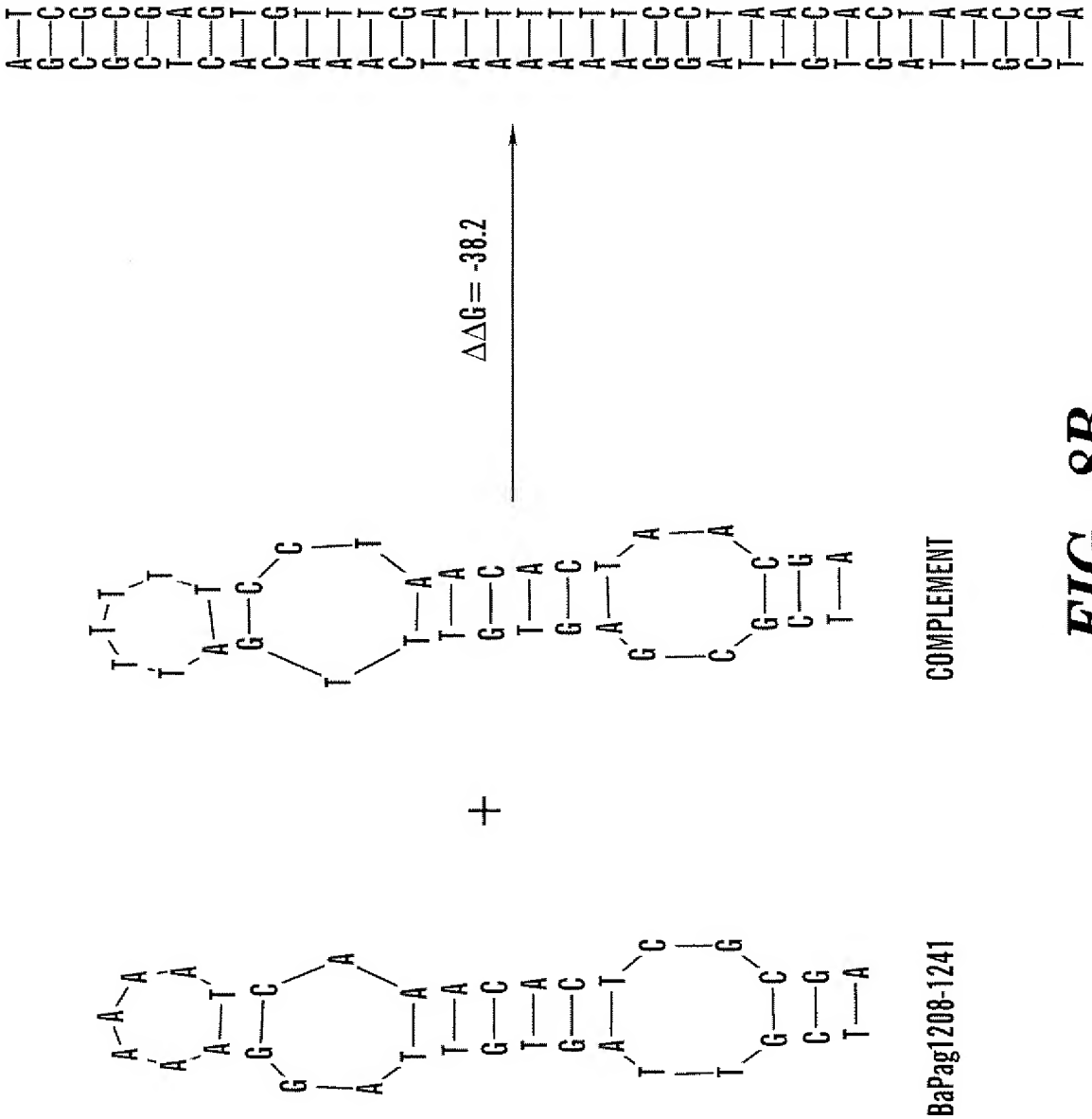


FIG. 8B

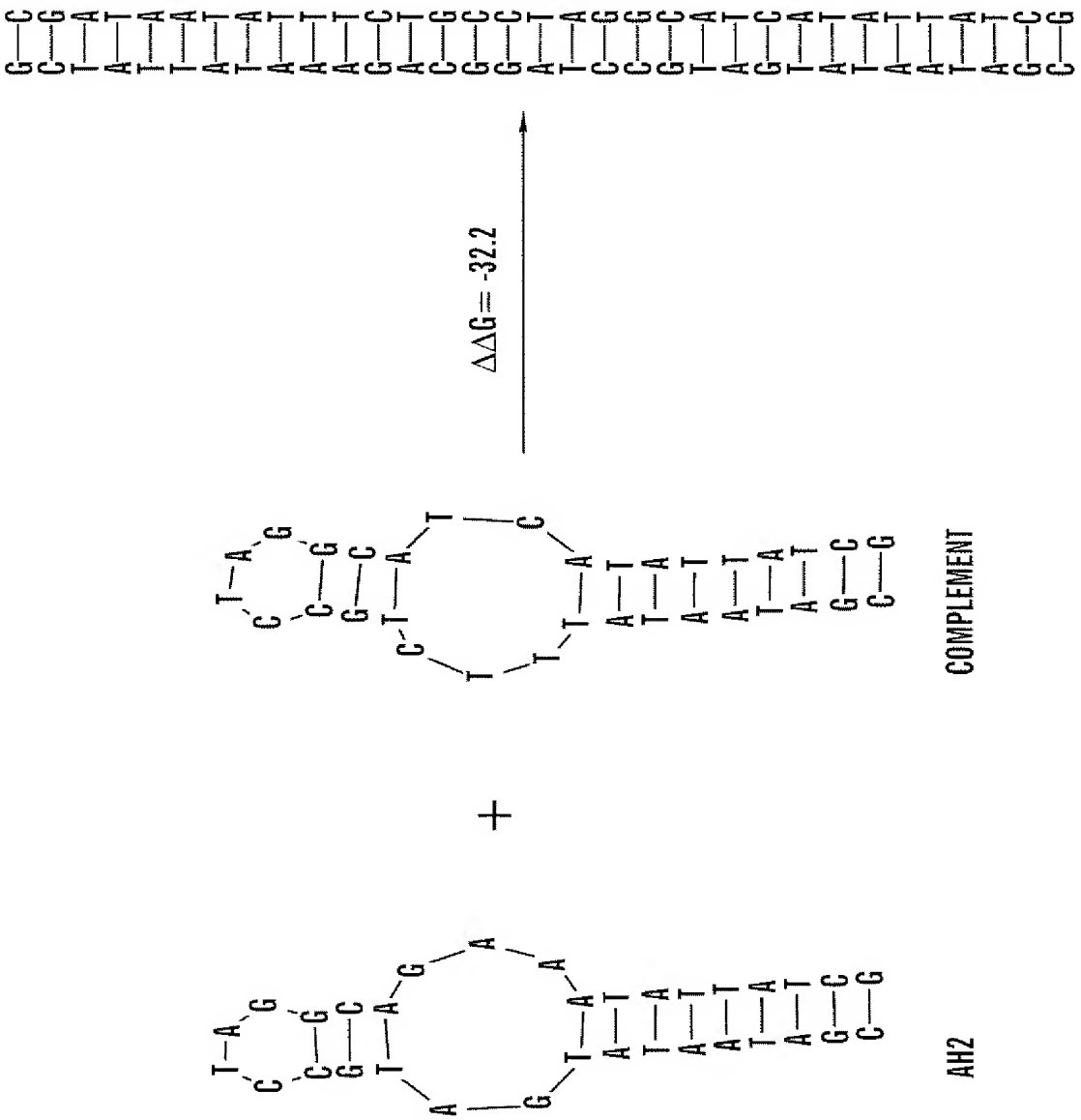


FIG. 8C

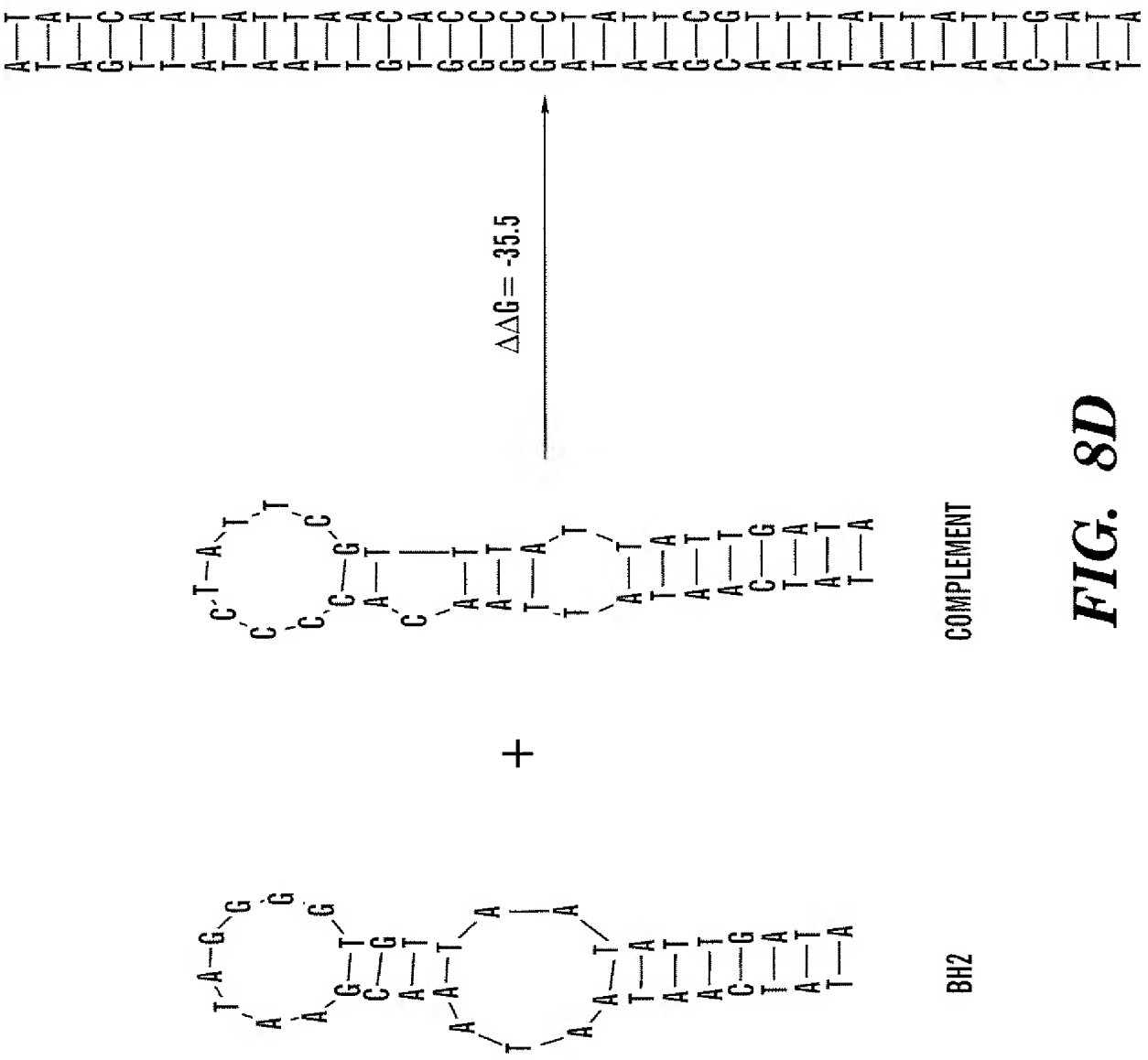


FIG. 8D

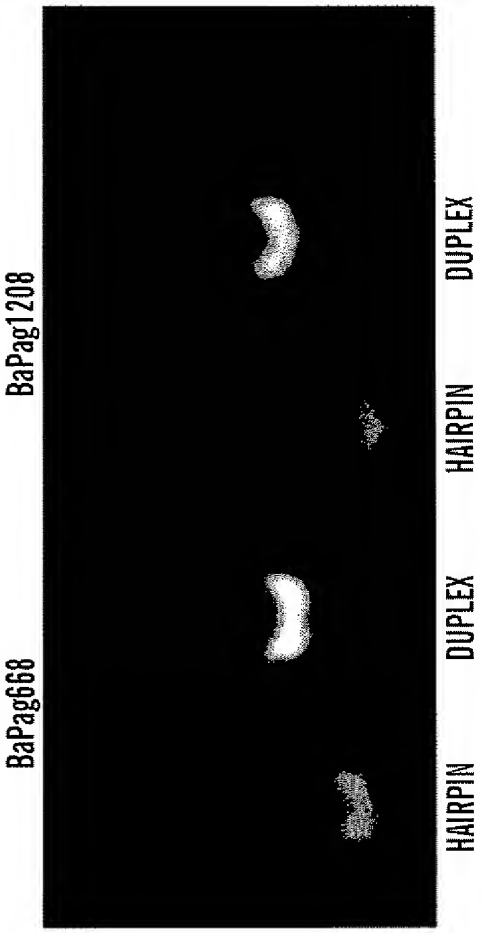


FIG. 9

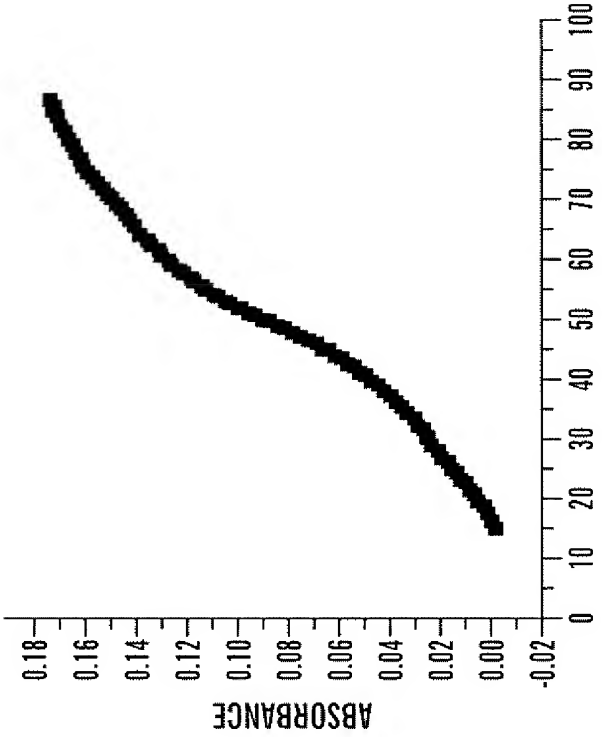


FIG. 10B

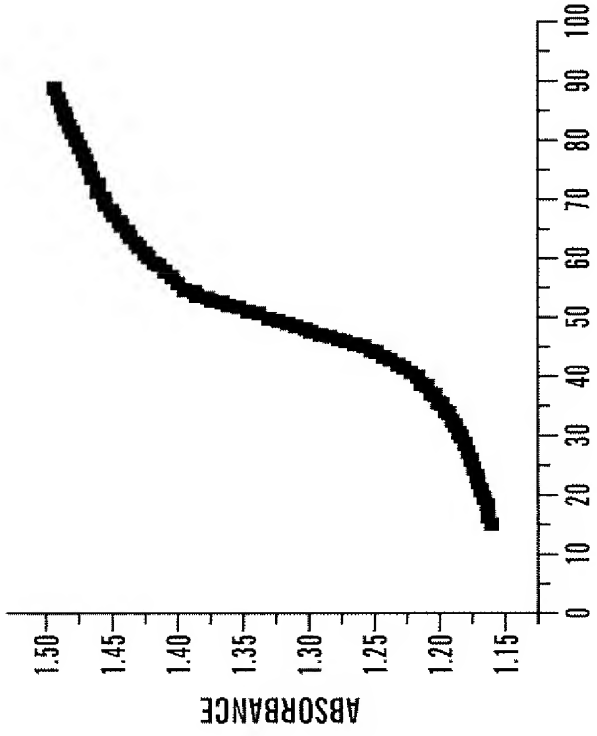


FIG. 10A

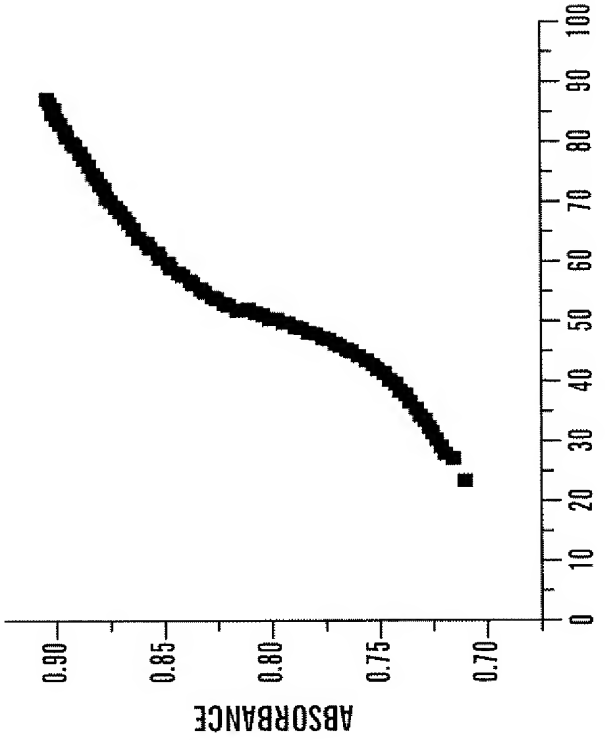


FIG. 10D

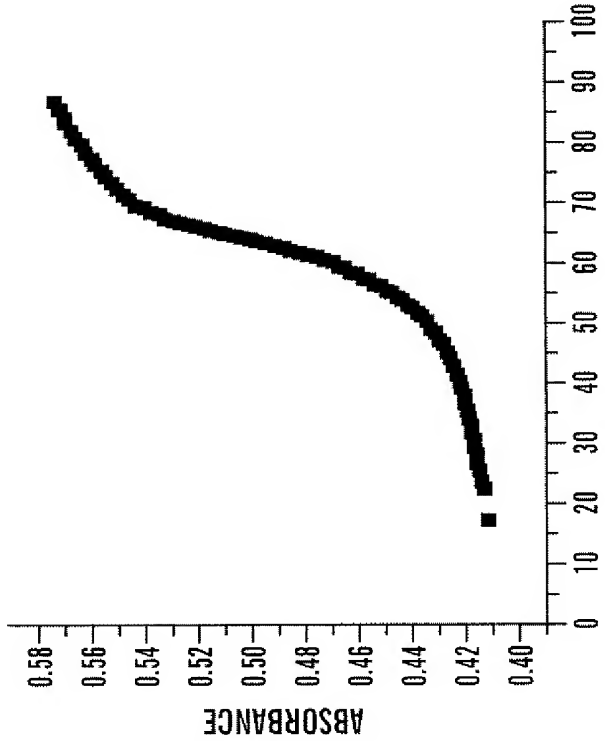


FIG. 10C

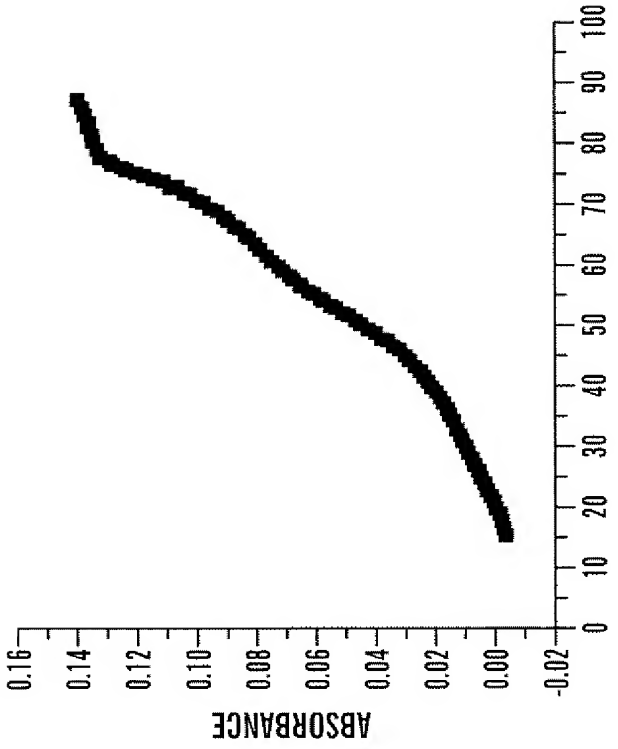


FIG. 10F

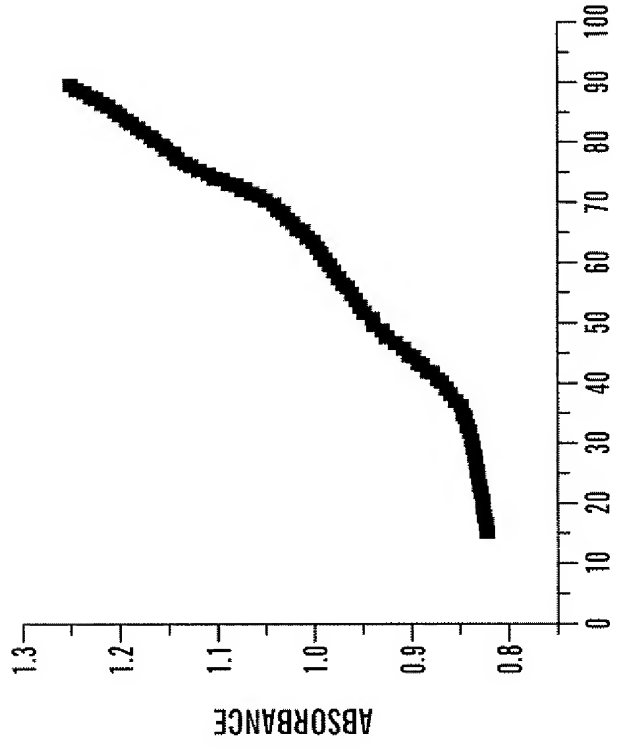


FIG. 10E

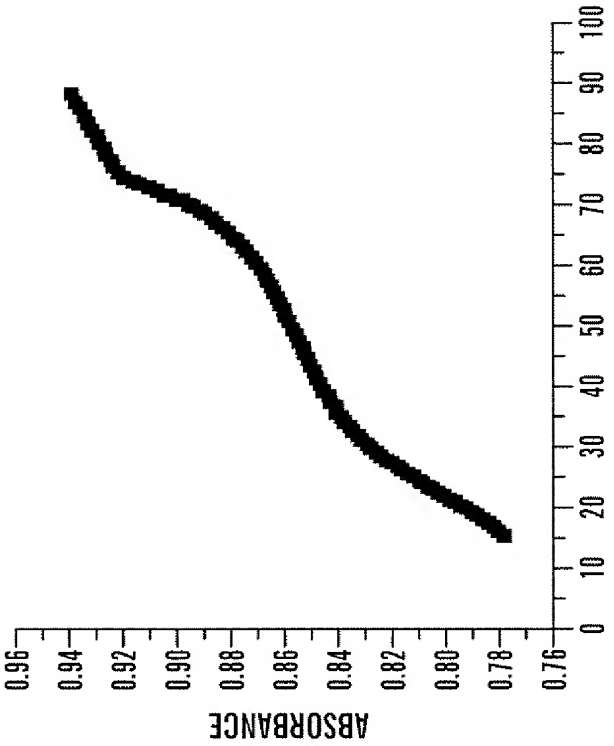


FIG. 10H

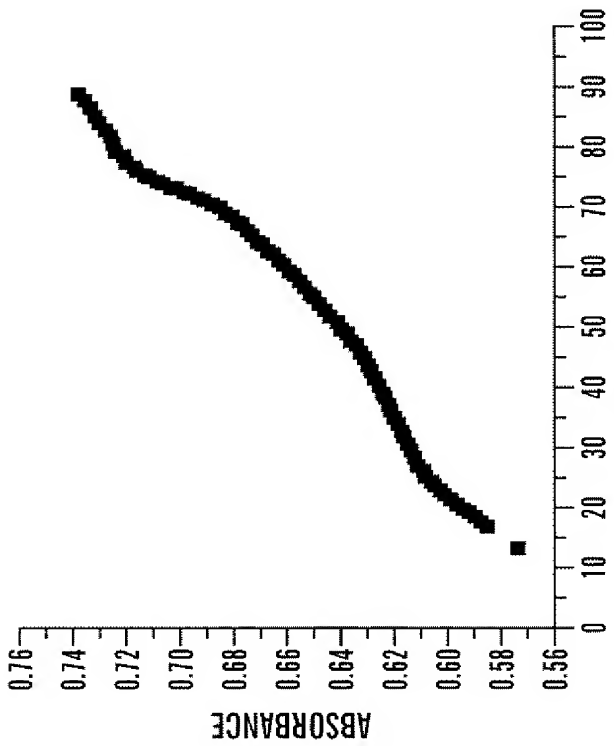


FIG. 10G

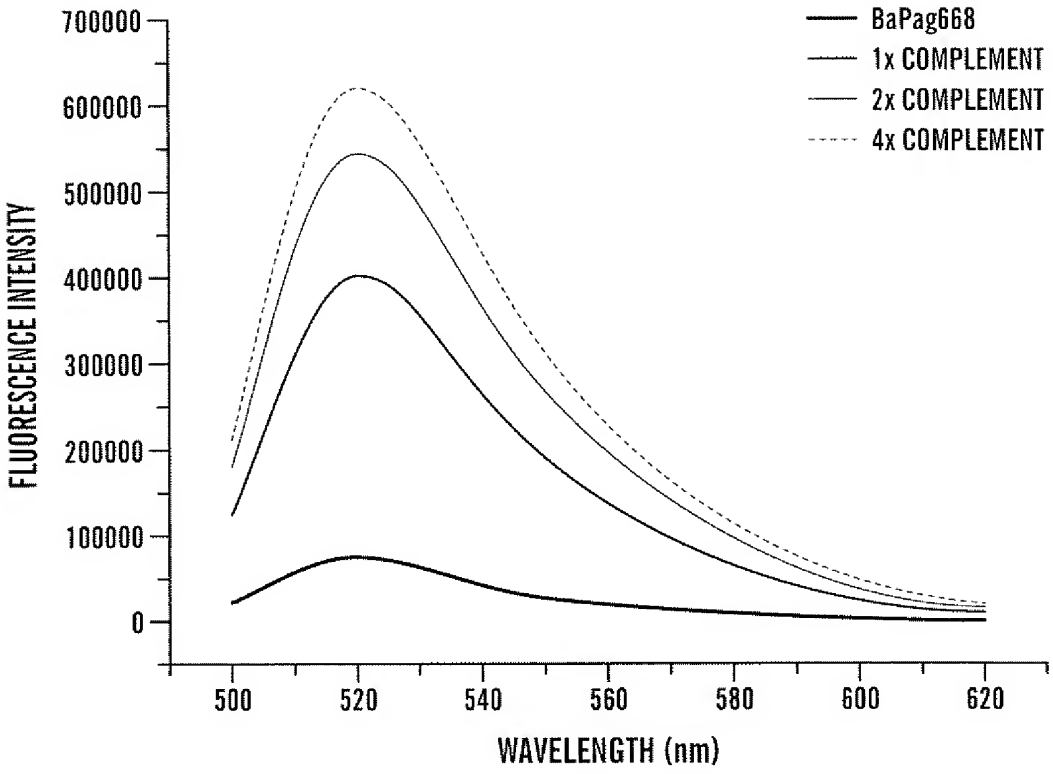

700000
600000
500000
400000
300000
200000
100000
0
FLUORESCENCE INTENSITY
500
520
540
560
580
600
620
WAVELENGTH (nm)
BaPag668
1x COMPLEMENT
2x COMPLEMENT
4x COMPLEMENT

FIG. 11

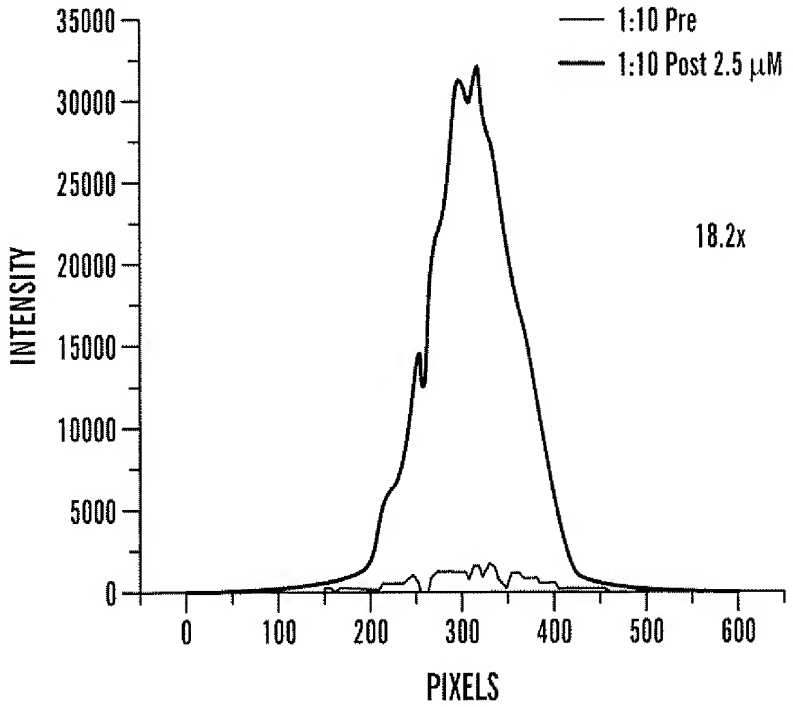


FIG. 12A

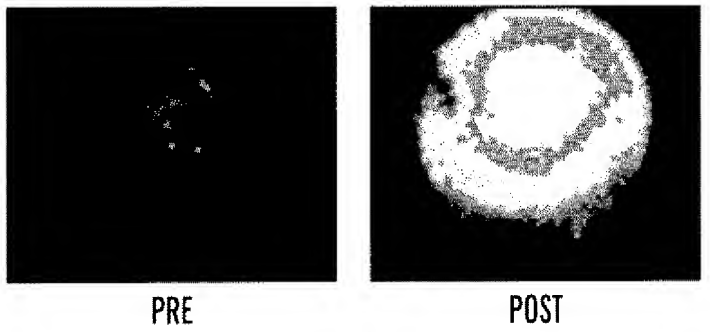


FIG. 12B FIG. 12C

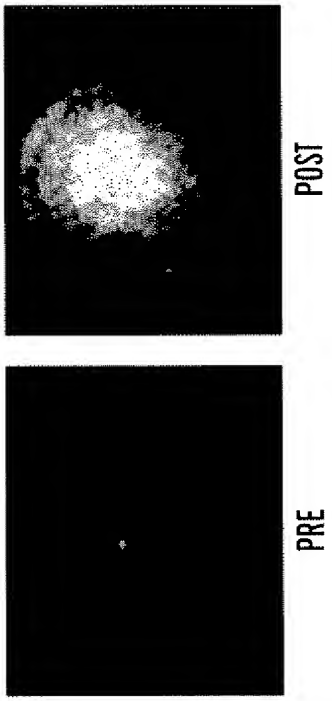


FIG. 12E

FIG. 12F

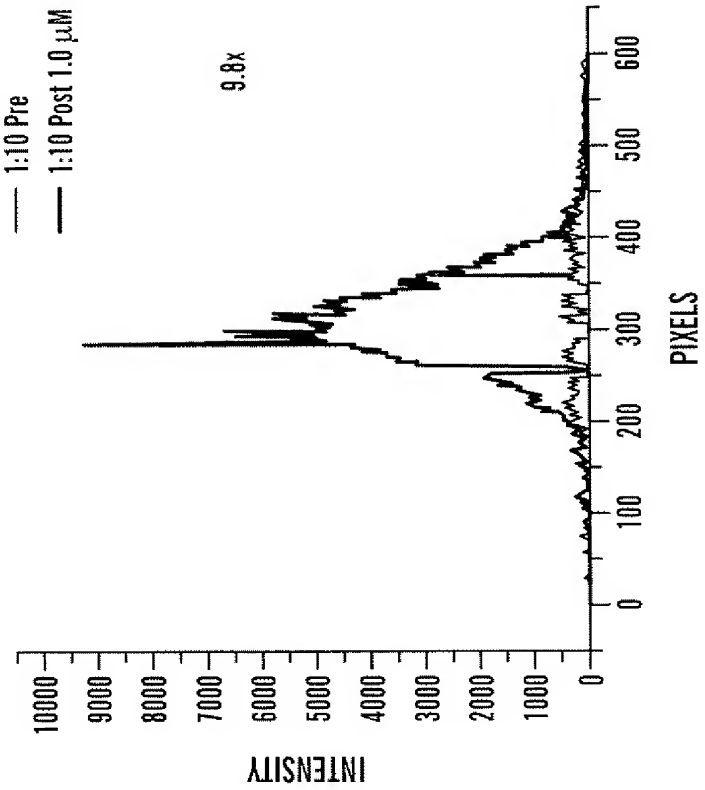


FIG. 12D

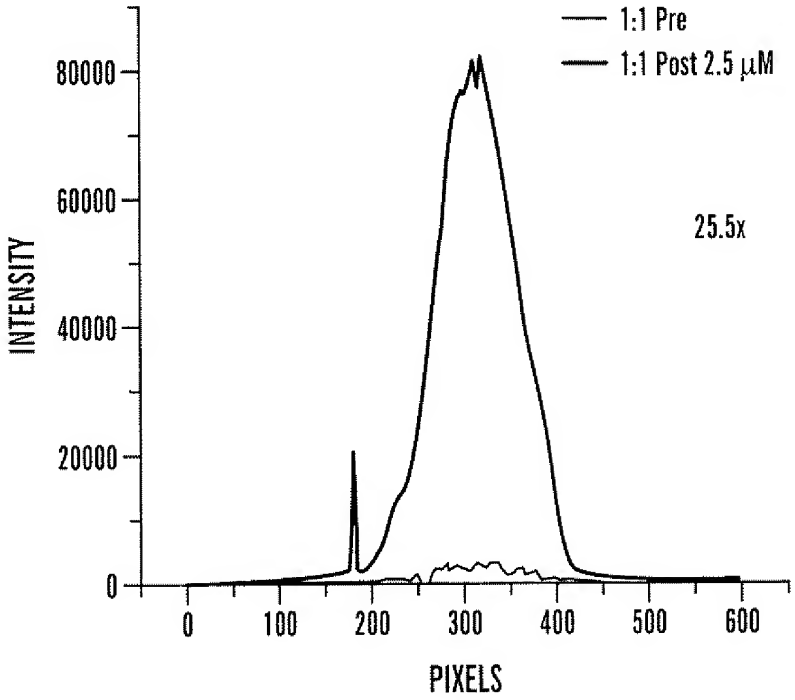


FIG. 13A

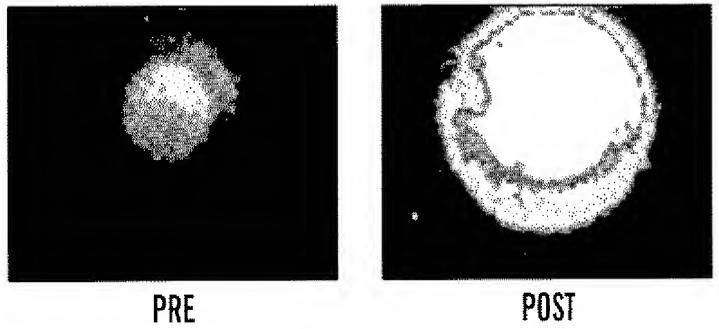


FIG. 13B *FIG. 13C*

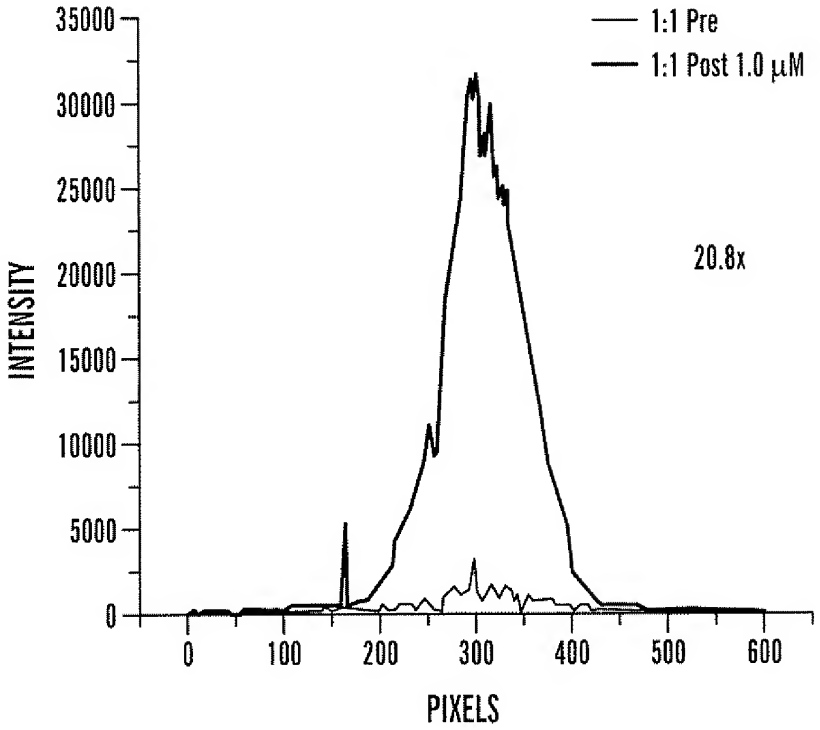


FIG. 13D

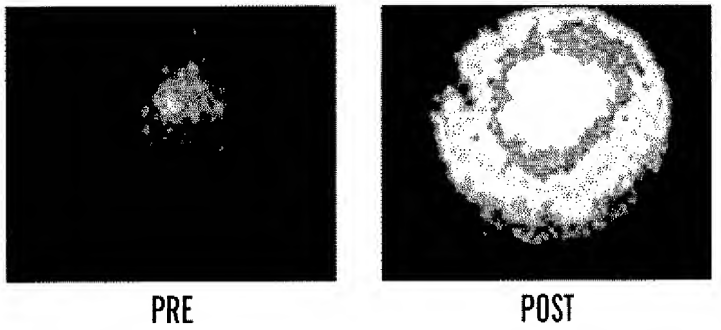


FIG. 13E FIG. 13F

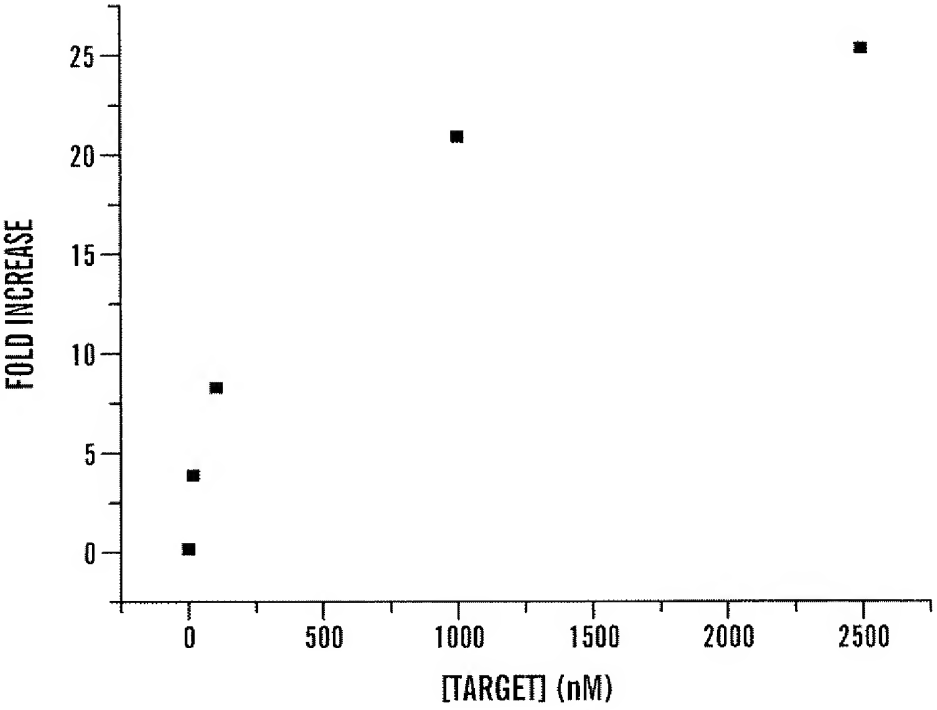

FOLD INCREASE
25
20
15
10
5
0
0
500
1000
1500
2000
2500
[TARGET] (nM)

FIG. 14

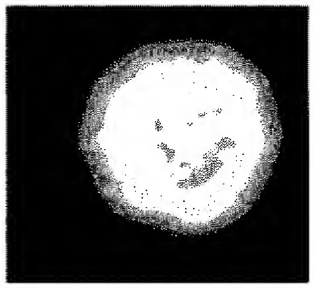


FIG. 15C

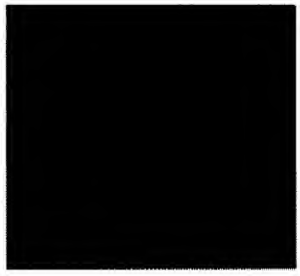


FIG. 15B

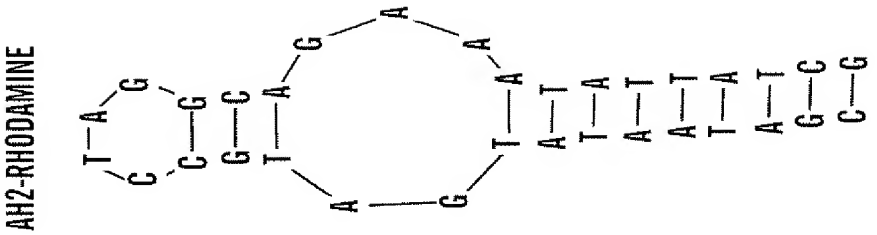


FIG. 15A

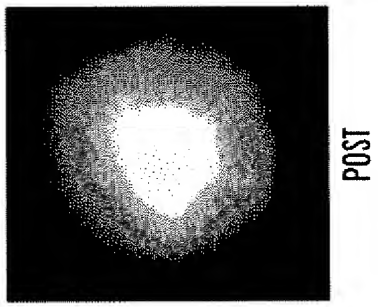


FIG. 15F

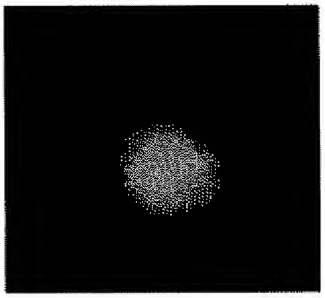


FIG. 15E

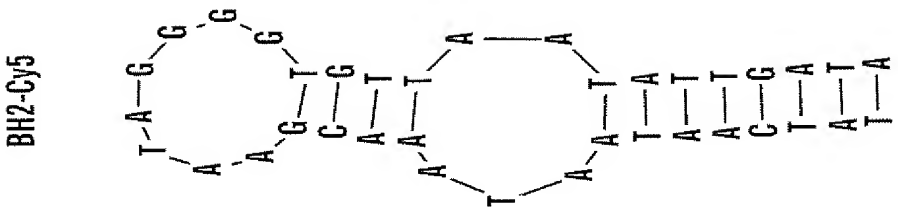
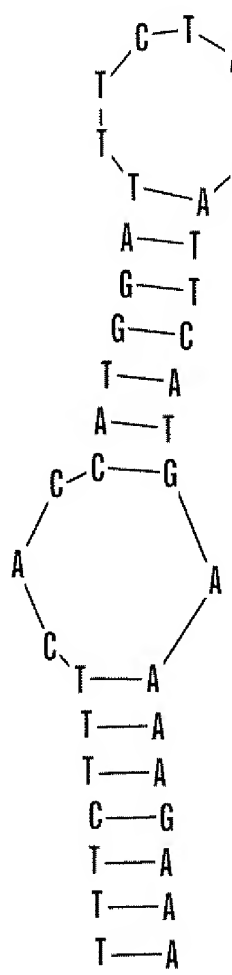
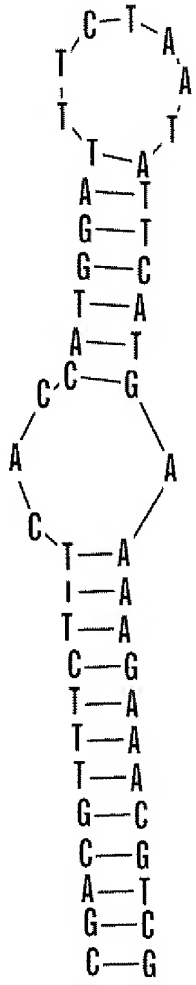


FIG. 15D



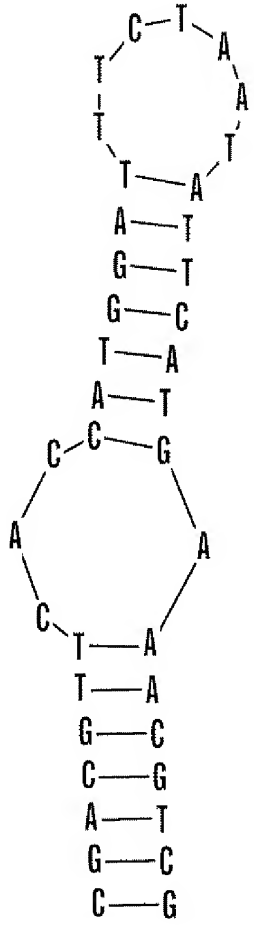
BaPag668
ΔG_{hp} = -4.4
ΔG_{dup} = -43.2
$\Delta\Delta G$ = -38.8

FIG. 16A



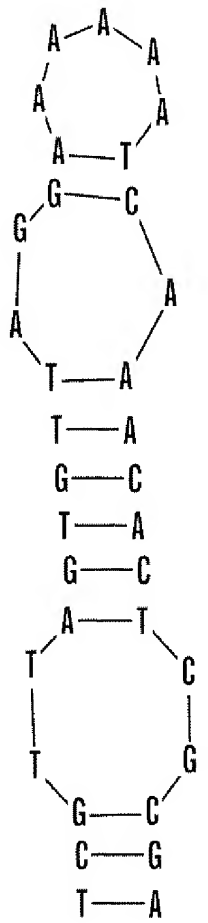
BaPag668+CGACG
ΔG_{hp} = -12.9
ΔG_{dup} = -43.2
$\Delta\Delta G$ = -30.3

FIG. 16B



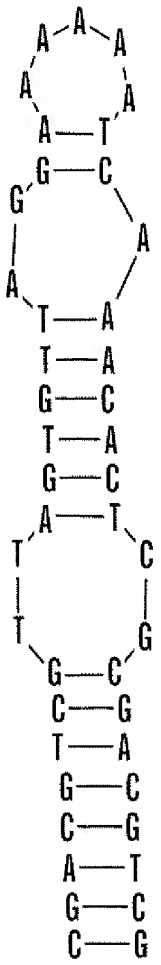
BaPag673+CGACG
ΔG_{hp} = -7.3
ΔG_{dup} = -32.5
$\Delta\Delta G$ = -25.2

FIG. 16C



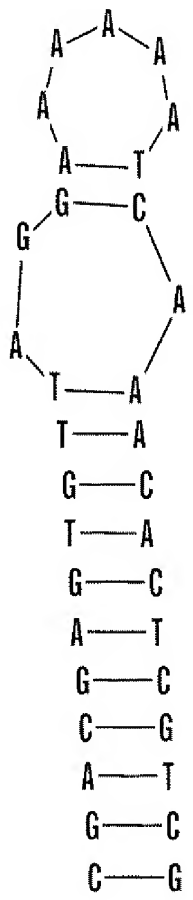
BaPag1208
ΔG_{hp} = -4.7
ΔG_{dup} = -42.6
$\Delta\Delta G$ = -38.2

FIG. 17A



BaPag1208+CGACG
ΔG_{hp} = -13.2
ΔG_{dup} = -42.8
$\Delta\Delta G$ = -29.6

FIG. 17B



BaPag1213+CGACG
ΔG_{hp} = -11.3
ΔG_{dup} = -33.7
$\Delta\Delta G$ = -22.4

FIG. 17C